Conformational flexibility of hybrid [3]- and [4]-rotaxanes

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ABSTRACT: The synthesis, structures and properties of [4]- and [3]-rotaxane complexes are reported where [2]rotaxanes, formed from heterometallic {Cr_7Ni} rings, are bound to a fluoride-centered {$CrNi_2$} triangle. The compounds have been characterized by single crystal X-ray diffraction and have the formulae $[CrNi_2(F)(O_2C^tBu)_6]\{(\mathbf{B}H)[Cr_7NiF_8(O_2C^tBu)_{16}]\}_3$ (**3**) and $[CrNi_2(F)(O_2C^tBu)_6(THF)]\{(\mathbf{B}H)[Cr_7NiF_8(O_2C^tBu)_{16}]\}_2$ (**4**); where **B** = py-$CH_2CH_2NHCH_2C_6H_4SCH_3$. The [4]rotaxane **3** is an isosceles triangle of three [2]rotaxanes bound to the central triangle while the [3]rotaxane **4** contains only two [2]rotaxanes bound to the central triangle. Studies of the behavior of **3** and **4** in solution by small angle X-ray scattering (SAXS) and atomistic molecular dynamic simulations (AMDS) show that the structure of **3** is similar to that found in the crystal but that **4** has a different conformation to the crystal. C.w. and pulsed EPR spectroscopy were used to study the structures present and demonstrate that in frozen solutions (at 5 K) **4** forms more extended molecules than **3** and with a wider range of conformations.

Introduction

The flexibility of supramolecular assemblies has long been of interest. For example, the rigidity of molecular capsules has been used to allow them to act as reactors to catalyse specific reactions[1] or to stabilise reactive species.[2,3] Interlocked structures such as the various knots reported[4-6] also introduce rigidity and have been proposed as means of making less flexible polymers.[7] Studying rigidity is possible using NMR spectroscopy where the species is diamagnetic; for example, the demetallated knots made by Zhang *et al* show broad NMR spectra that become sharper when diamagnetic Zn^{2+} ions are added which increases the rigidity. Studying the flexibility of interlocked structures where building blocks are paramagnetic is far harder as the NMR is paramagnetically broadened before the conformational flexibility is considered. Small angle X-ray scattering (SAXS) has been previously used to show supramolecular assemblies are present in solution;[8, 9] we have used SAXS supported by atomistic molecular dynamics simulations (AMDS) to demonstrate that a [13]rotaxane maintained its structure in solution.[10] Here we use SAXS on two related rotaxanes to show that the larger [4]rotaxane has a more similar structure between solution and crystalline phases, while a [3]rotaxane has a much more open structure in solution. The studies require the comparison of SAXS and double electron-electron resonance (DEER) spectroscopy while remembering they operate at 300 and 5 K, respectively.

We have previously reported hybrid [2]rotaxanes where the ring is a $[Cr_7NiF_8(O_2C^tBu)_{16}]^-$ unit and the thread is a secondary ammonium with suitable sterically-demanding stoppers.[11, 12] If there is a pyridyl (py) head group on the thread, for example py-$CH_2NHCH_2CH_2Ph$ (**A**), the [2]rotaxane $(\mathbf{A}H)[Cr_7NiF_8(O_2C^tBu)_{16}]$ can be used to bind to Lewis acid complexes.[13, 14] Here we extend this approach, binding [2]rotaxanes to a fluoride-centred triangle $[CrNi_2(\mu_3\text{-}F)(O_2C^tBu)_6(HO_2C^tBu)_3]$ **1** (Figure S2) which has a labile terminal ligand (HO_2C^tBu) at each vertex. By small changes in the synthesis [3]- and [4]-rotaxanes can be made and which show very different solution flexibility.

Such assemblies have been proposed as routes to implement qubit gates. Both the {Cr_7Ni} ring and the {$CrNi_2$} triangle have S = ½ ground states, but with very different g-values of *ca.* 1.8 and 2.5.[15] This gives supramolecular assemblies where we can potentially address different components by EPR spectroscopy. This has also been investigated.

Results: Synthesis and Structural Analysis

The parent {$CrNi_2$} triangle $[CrNi_2(\mu_3\text{-}F)(O_2C^tBu)_6(HO_2C^tBu)_3]$ (**1**; Figure S2) was prepared as reported previously.[15] Attempts to coordinate $(\mathbf{A}H)[Cr_7NiF_8(O_2C^tBu)_{16}]$[13] to **1**, were unsuccessful probably due to the thread being too short, leading to repulsive steric interactions between the components. Hence, we made py-$CH_2CH_2NHCH_2C_6H_4SCH_3$ (**B**) which has a greater distance between the secondary amine site and the pyridyl head group.[16] A [2]rotaxane can then be prepared, of formula $(\mathbf{B}H)[Cr_7NiF_8(O_2C^tBu)_{16}]$ (**2**); the thread is protonated at the amine site during this reaction (Figure S3).

Reaction of three equivalents of **2** with **1** in THF at 40 °C produces the 3:1 {Cr_7Ni}:{$CrNi_2$} adduct $[CrNi_2(F)(O_2C^tBu)_6]\{(\mathbf{B}H)[Cr_7NiF_8(O_2C^tBu)_{16}]\}_3$ **3** (Figure 1a) as shown by X-ray diffraction. The structure contains three molecules of **2** each bound to a metal site of the central triangle **1** *via* the py head groups of the $(\mathbf{B}H)^+$ threads. Compound **3** is

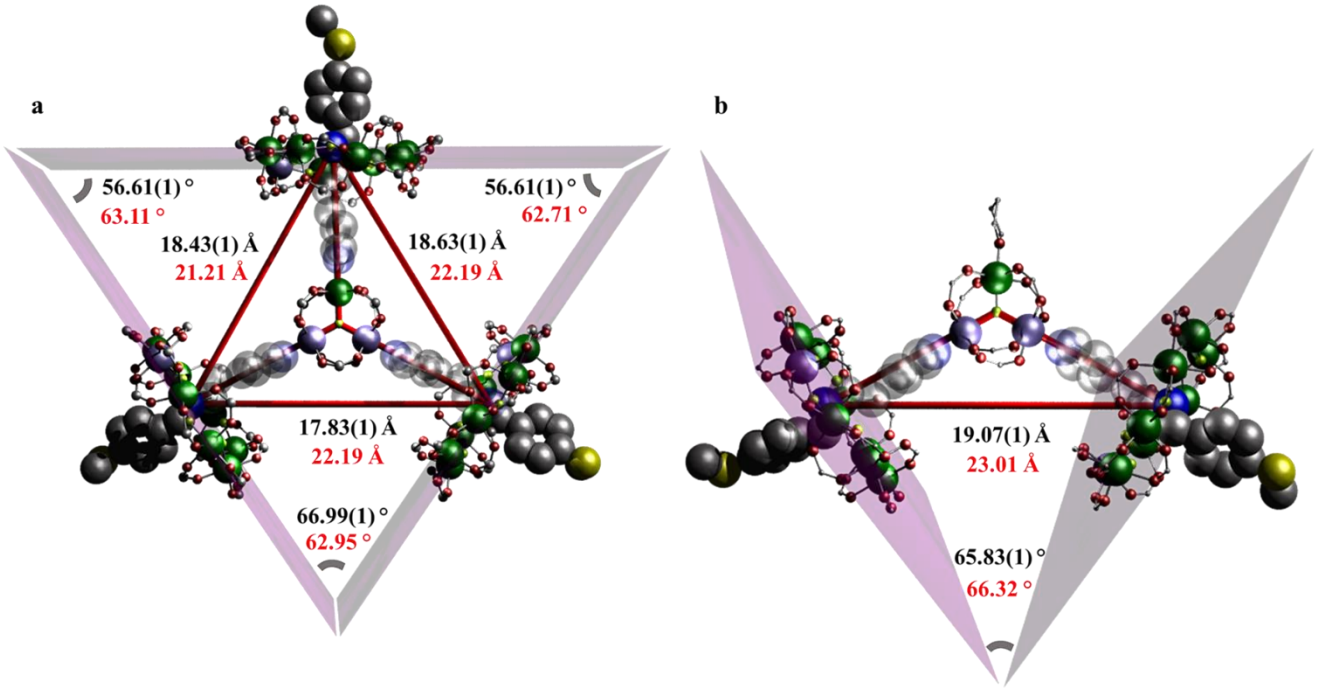

Figure 1. The structures of **3** and **4** in the crystal, with select metric parameters indicated (black, XRD; red, AMDS). (a) **3** showing angles between the mean planes of the {Cr_7Ni} rings, and the distances between N atoms of secondary ammonium groups; (b) **4** showing angles between the mean planes of the {Cr_7Ni} rings and the distances between N atoms of secondary ammonium groups. Colors: Cr, green; Ni, purple; O, red; F, yellow; N, blue; C, silver; S, dull yellow. H-atoms and methyl groups of pivalates excluded for clarity.

therefore a [4]rotaxane. It crystallises with a 2-fold axis of rotation passing through the molecule and therefore the asymmetric unit comprises half of the complete molecule.

In the central {$CrNi_2$} triangle each metal ion is in a *pseudo*-octahedral geometry, with the pyridyl bound *trans* to the central μ_3-fluoride, which is planar (Ni-F-Cr and Ni-F-Cr angles all around 120°). In the solid state, the pyridyl groups are almost perpendicular to the {$CrNi_2$} plane; angles between the py and {$CrNi_2$} planes vary from 75.14(1) – 80.88(1)°. Each {Cr_7Ni} ring sits about the secondary ammonium group (N^{am}) of (**B**H)$^+$, with hydrogen bonds to two of the bridging fluorides on the interior of the ring.

The Cr^{III} site in the triangle is disordered over the three sites. Similarly, in the {Cr_7Ni} rings the Ni^{II} site is disordered over all eight metal positions. Although elemental analysis gives a slight excess of Ni with a Ni:Cr ratio of 6:22 (5:22 expected for a **2**:{$CrNi_2$} ratio of 3:1), EPR spectroscopy unequivocally demonstrates that there is no scrambling of the metal ions, i.e. all the rings are {Cr_7Ni} and all the triangles are {$CrNi_2$} (see below).

Table 1. Metric parameters defining the shape of the [n]rotaxanes

	3		**4**	
	X-ray	AMDS	X-ray	AMDS
N^{am}..F distance/ Å	10.56(1) 10.57(1) 10.57(1)	10.31(1) 10.31(1) 10.31(1)	10.82(1) 10.84(1)	10.31(1) 10.31(1)
N^{am}..N^{am} distance/ Å	17.83(1) 18.43(1) 18.83(1)	21.21(1) 21.21(1) 22.19(1)	19.07(1)	23.01(1)
Ring..ring angle/ °	56.61(1) 56.61(1) 66.99(1)	62.71(1) 62.95(1) 63.11(1)	65.83(1)	66.32(1)

If the reaction is carried out using two equivalents of **2** to **1** and in THF at 20 °C, we isolate the 2:1 {Cr_7Ni}:{$CrNi_2$} adduct where only two sites of **1** have been substituted by **2** and the third site is occupied by a THF molecule. The product is a [3]rotaxane [$CrNi_2(F)(O_2C^tBu)_6(THF)$]{(**B**H)[$Cr_7NiF_8(O_2C^tBu)_{16}$]}$_2$ (**4**; Figure 1b). X-ray diffraction shows that the THF substituted metal site of the {$CrNi_2$} triangle has a shorter M-F bond distance of 1.89(3) Å *cf.* 2.06(1) and 2.06(1) Å and hence the Cr^{III} site is localised. The μ_3-F^- of the triangle is again planar with Ni-F-Cr and Ni-F-Cr angles near 120°. The planes of the py groups are almost perpendicular to the {$CrNi_2$} plane, with dihedral angles of 77.48(1) and 84.04(1)°, which are similar to those of **3**.

To define the shape of the two supramolecules we report some simple metric parameters (Figure 1, Table 1). Firstly, we consider the distance from the central fluoride in each case to the protonated secondary ammonium in each thread about which the {Cr_7Ni} rings are grown: this is the N^{am}…F distance for each thread. We then consider the N^{am}…N^{am} distances; these define the edges of the triangle of {Cr_7Ni} rings in **3**. The angles between the mean planes of the {Cr_7Ni} rings on each [2]rotaxane are given as the ring…ring angles. In each case the mean plane of the ring is essentially perpendicular to the thread passing through it.

The X-ray diffraction results show that **3** contains an approximately isosceles triangle of {Cr_7Ni} rings, with one ring…ring angle noticeably more obtuse than the other two. The N^{am}…F distances are constant. For **4** the angle between the two rings is similar to the most obtuse angle for **3** and the N^{am}…N^{am} and N^{am}…F distances are both longer than in **3**.

Atomistic Molecular Dynamic Simulations (AMDS) and Small Angle X-ray Scattering (SAXS)

To study the stability and structures of **3** and **4** in solution atomistic molecular dynamic simulations (AMDS) were performed with an all-atom simulation of the two crystal structures (in a concentrated THF solution) using GROMACS 5.1.4 molecular dynamics package.[17, 18] The crystal structures of **3** and **4** were parameterised using the AMBER95 forcefield, augmented by parameters consistent with the General Amber forcefield.[19] 8 nm cubic simulation boxes were set up containing a single molecule of **3** or **4** in a solution of 2774 THF molecules and run in an NPT ensemble for the solvent density to reach ~890 kg m^{-3}.

The calculated AMDS structures were then compared with experimental solution structure information from SAXS data. SAXS profiles calculated from the AMDS structures used Hartree-Fock scattering factors, with 100 nm boxes and X-ray wavelength of 0.154209 nm. Experimental and AMDS-model calculated SAXS intensity profiles (plotted as ln[$I(q)$] (a.u.), where q (Å) is the scattering vector) are in Table S2 and Figure S12. The corresponding pair distribution functions P(r) for **3** and **4** are in Figure 2.

There is remarkable agreement between AMDS and SAXS for both **3** and **4**, demonstrating that both structures are stable in THF solution (Figure 2). The very slight discrepancies between the experimental SAXS and corresponding pair distribution function is less than 1 Å, for both **3** and **4**, which can be accountable by forcefield errors. This discrepancy is also seen in the radius of gyration (Rg) values shown in Table S2. The radius of gyration for the simulated structures of both **3** and **4** are slightly higher indicating the calculated structures are more extended in comparison to the experimental data.

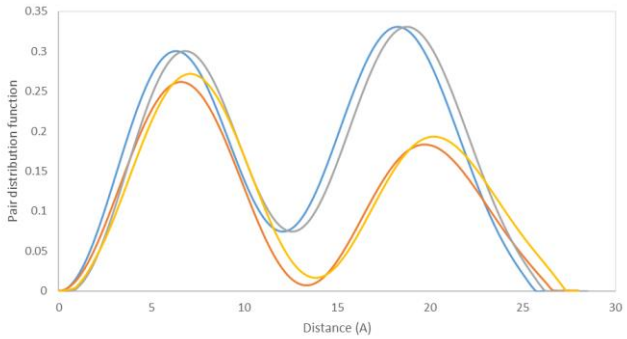

Figure 2. Observed and calculated SAXS data for **3** and **4**, in THF solution at 20 °C. The experimental data is shown in blue and red, respectively, for **3** and **4**. The calculated traces are shown in grey and yellow, respectively, for **3** and **4**.

The P(r) distributions are dominated by a short distance (ca. 6 Å) and a longer distance at ca. 18 and 20 Å for **3** and **4**, respectively. The longer distance can be attributed to the distances between {Cr_7Ni} rings. Note that this inter-ring distribution has greater amplitude for **3** than for **4**, consistent with the 3:1 vs. 2:1 {Cr_7Ni}:{$CrNi_2$} stoichiometries. The shorter distances within the peak centered at *ca.* 7 Å are due to distances within individual {Cr_7Ni} rings, agreeing with the crystallographic values that range from 3.3(1) Å (neighboring sites) to 8.7(1) Å (antipodal sites). The combination of AMDS/SAXS confirm that **3** and **4** are distinct compounds in solution and, for example, **3** does not exist in equilibrium with **4** and a dissociated [2]rotaxane **2**.

The AMDS structures calculated by molecular dynamics are also in good agreement with the single crystal structures (see Table 1 for selected metric parameters) but with some subtle and intriguing variations. Compound **3** is noticeably more equilateral in solution, with the ring…ring angles all very similar. While the three angles in the crystal structure sum to close to 180°, in the AMDS structure they sum to an average of 189° over the last 5 ns of the simulations, which corresponds to the rings tilting away from the normal to the {$CrNi_2$} plane in solution. The N^{am}…F distances are shorter but N^{am}…N^{am} distances are 17% longer. These observations indicate that the rings are packed together more closely than they would like in the crystal and the structure relaxes in solution. Compound **4** has a very similar ring…ring angle in solution and crystal structure (Table 1) but the N^{am}…N^{am} distance is 20% longer in solution than in the crystal. This again suggests that the structure in the solution has relaxed compared with the crystal structure.

Electron Paramagnetic Resonance Spectroscopy

Continuous Wave (c.w.) Q-band (ca. 34 GHz) EPR spectroscopy measurements were performed on **3** and **4** at 5 K for powder samples and for frozen 3 mM toluene solutions. The spectra are dominated by the S = ½ ground states of the {Cr_7Ni} and {$CrNi_2$} components, that arise from internal antiferromagnetic coupling.

The powder spectra for **3** and **4** (Figure S4; left and right, respectively) both contain two slightly asymmetric features, centred on 995 and 1382 mT. The frozen solution spectra (Figure 3) have narrower linewidths, which for both **3** and **4** reveal approximately axial splitting of the lower field feature, while the higher field feature remains largely unchanged. The spectra were simulated[20] using a spin-Hamiltonian incorporating only the individual g-matrices for the S = ½ {$CrNi_2$} and {Cr_7Ni} components and an isotropic exchange interaction:

$$\hat{H} = \mu_B \hat{S}^{CrNi2} \cdot \mathbf{g}^{CrNi2} \cdot \mathbf{B} + \Sigma \mu_B \hat{S}^{Cr7Ni} \cdot \mathbf{g}^{Cr7Ni} \cdot \mathbf{B} - 2J\Sigma \hat{S}^{CrNi2} \cdot \hat{S}^{Cr7Ni}$$

where the summation is over three (compound **3**) or two (compound **4**) {Cr_7Ni} centres.

For the frozen solutions, the lower field feature due to {$CrNi_2$} can be fitted with: for **3**, $g_{x,y,z}$ = 2.425, 2.425, 2.520; for **4**, $g_{x,y,z}$ = 2.420, 2.425, 2.515. These agree well with the spectra found for **1**.[15] The high field feature due to {Cr_7Ni} can be fitted with: **3**, $g_{x,y,z}$ = 1.785, 1.778, 1.730 ; and **4**, $g_{x,y,z}$, = 1.782, 1.782, 1.740. These agree with the spectra of {Cr_7Ni} rings.[21] Reasonable fits can be achieved with these g-values for J = 0.

A slight improvement in the agreement between the simulated and observed spectra is found with the inclusion of a small exchange interaction of $|J|$ = 0.003 cm^{-1}. However, this only serves to broaden the transitions. This broadening can also be achieved by inclusion of a small (1%) g-strain for each {Cr_7Ni} component. Frozen solution spectra of **3** at lower frequencies

(X- and S-band) fit better with the *g*-strain model than with the small, but unresolved *J* model (Figure S5). We conclude that there are no measurable features due to exchange coupling in the c.w. EPR spectra.

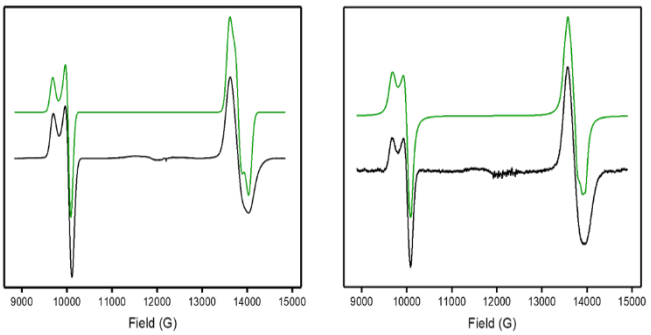

Figure 3. c.w. Q-Band EPR (ca. 34 GHz) spectra for a 3 mM solution sample in dry toluene for **3** (left) and **4** (right) at 5 K. Black: experimental, and green: simulation.

Pulsed EPR spectroscopy (Q-band, 3 K) was used to measure the phase memory times (T_m) for **3** and **4** using standard Hahn echo decay measurements: [π/2-τ-π-τ-echo]. Spin lattice relaxation (T_1) measurements were carried out by inversion recovery [π-*T*-π/2-τ-π-τ-echo]. We have also done comparable measurements on the isolated triangle $[CrNi_2(F)(O_2C^tBu)_6(py)_3]$ **5**.[15] Measurements were made at magnetic fields (B_0) corresponding to resonances of the {Cr_7Ni} ring and the g_{xy} and g_z features for the {$CrNi_2$} triangle (Table 2 and Figure S6). The phase memory (T_m) times are similar for all components in both structures at around 700 ns, with the exception of the g_z values for the {$CrNi_2$} fragment in **3** and **4** which is shorter (*ca.* 570 ns), and shorter than in the isolated {$CrNi_2$} triangle **5**. The T_1 times vary more and the times for the isolated triangle are significantly longer than for the {$CrNi_2$} *g*-values in **3** and **4** (Table 2 and Figures S7, S9).

Table 2. Q-band relaxation times for **3**, **4** and **5** measured at 3 K in 0.2 mM solution in toluene.

Compound	*g*-value	Assignment	T_m/ns	T_1/ μs
3	2.41	g_{xy} {$CrNi_2$}	713 (0.42)	172 (0.38)
3	2.47	g_z {$CrNi_2$}	562 (2.96)	108 (1.78)
4	2.41	g_{xy} {$CrNi_2$}	689 (2.46)	258 (3.34)
4	2.47	g_z {$CrNi_2$}	578 (3.61)	165 (1.43)
5	2.41	g_{xy} {$CrNi_2$}	863 (0.4)	840 (17)
5	2.47	g_z {$CrNi_2$}	848 (0.5)	813 (24)
3	1.78	{Cr_7Ni}	713 (0.42)	62 (0.38)
4	1.78	{Cr_7Ni}	826 (0.56)	108 (0.75)

ESEEM modulations are observed in the Hahn echo decay measurements at B_0 values corresponding to the {$CrNi_2$} but not for the {Cr_7Ni} components. Fourier transforms of the time-domain data for the {$CrNi_2$} measurements are similar for **3** and **4**, with series of low-frequency (< 10 MHz) peaks (Figure S8).

Double Electron-Electron Resonance Spectroscopy (DEER)

DEER is an established method for measuring inter-spin distances in biological systems.[22-24] Previously we have reported DEER measured on supramolecular compounds containing two {Cr_7Ni} rings and demonstrated that we could measure the weak {Cr_7Ni}…{Cr_7Ni} interactions.[25] In those studies the two rings were co-planar, linked along the normal to the planes of the rings, either by forming a [3]rotaxane, or linked covalently via a diamagnetic bridge. In **3** and **4** the planes of the rings make angles of ~60° to one another (see Table 1), which introduces a further structural complexity to interpreting the results.

Four-pulse DEER experiments were performed on solutions of **3** and **4** to probe the {Cr_7Ni}…{Cr_7Ni}interactions. The pump pulse was set on the {Cr_7Ni} maximum (B_0 = 1373 mT) with the observer pulse set 100 MHz higher in frequency than the pump pulse. For both compounds, we observe oscillations in the DEER traces (Figures 4 and 5). For **3**, Fourier transformation of the background corrected data gives a frequency domain spectrum with peaks at ±5 MHz, with a slight shoulder at ±3 MHz, and broad wings between ±10-30 MHz. For **4**, we obtain similar oscillations but with weaker modulation depth, giving a frequency domain spectrum with two distinct peaks at ±2.5 and ±5 MHz. There appears to be less intensity in the wings.

Two analysis methods were used to extract inter-spin distance distribution from the time traces. Firstly, a Tikhonov regularization[26] using the orientation independent kernel in DeerAnalysis,[27] with a correction for the *g*-values corresponding to the pump and detection frequencies, yields three main components for **3** (Figure 4c) and gives four clear groups of distances for **4** (Figure 5c).

Secondly, a simulation library approach was used (see SI). A series of geometric models were developed based on the crystal structures of **3** and **4**. For each model the expected orientation dependent DEER trace for pairwise ring-ring dipolar interactions was calculated using an algorithm described elsewhere.[28] The unpaired spin density in each {Cr_7Ni} was equally distributed on each metal ion, reflecting the fact that the Ni position in the ring is not localized. The calculations used the anisotropic *g*-values from c.w. spectra, and the mw pulse and magnetic field parameters used in the experimental acquisition. This library of simulated DEER traces was fitted to the experimental data traces using an iterative procedure over 50 iterations, similar to that described elsewhere.[29] The time and frequency domain fits and the corresponding distance distributions, presented as both the inter-ring M…M distances and ring centroid-to-centroid distances, are presented in Figures 4 and 5.

Power scaling of the DEER data for **3** was used to test for the presence of significant multi-spin effects and ghost peaks in the extracted distance distribution.[30] The contribution of the multi-spin effects to the data set is vanishingly small (see SI): this is because the inversion efficiency of the DEER experiment is very low (λ = 0.0135). This validates the application of the pairwise analysis approaches described above for **3**. The greater modulation depth for **3** than for **4** is consistent with the presence of three {Cr_7Ni} rings in the former and two in the latter.[31]

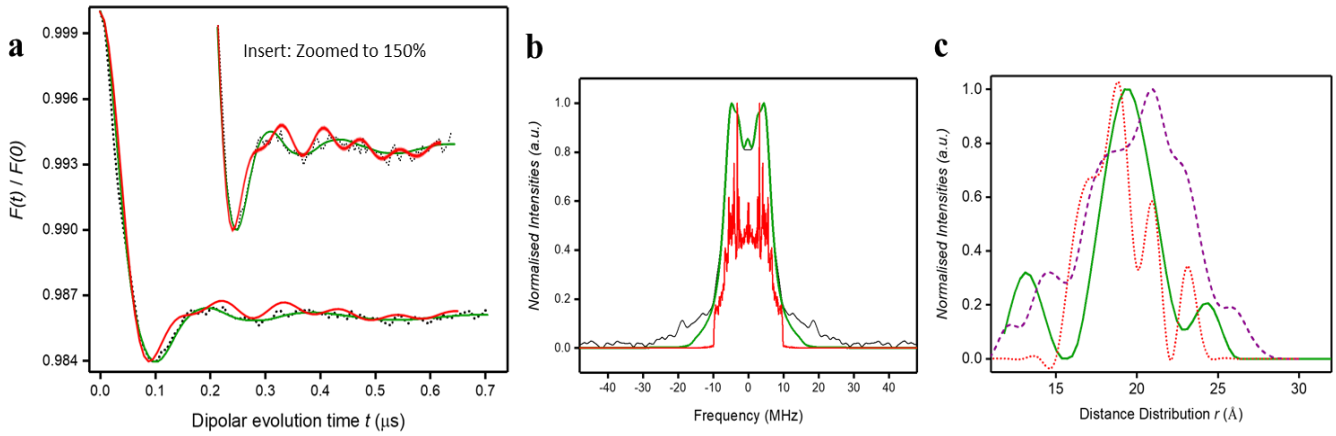

Figure 4. a) Q-Band experimental DEER trace of **3**, after background subtraction, (black crosses, 0.2 mM solution in dry and degassed toluene at 3 K) and fitted data; using DeerAnalysis (solid green line) and using an iterative orientation procedure (solid red line), with vertical enlargement (insert). A four-pulse DEER sequence was used, with the ELDOR pulse at the {Cr_7Ni} maximum (B_0 = 1373 mT) and observation pulse positioned at +100 MHz. Pulse lengths were 20 and 40 ns for π/2 and π, respectively, with τ_1 = 200 ns and τ_2 = 1000 ns. b) Pake pattern from Fourier transformation of dipolar evolution (solid black line); fitted data using DeerAnalysis (solid green line) and the iterative orientation procedure (solid red line). c) Distance distribution using Tikhonov regularizations in DeerAnalysis and corrected *g*-values (solid green line), and from the model from the iterative orientation procedure showing inter-ring metal-metal distances (dashed purple line) and ring centroid-centroid distances (dotted red line).

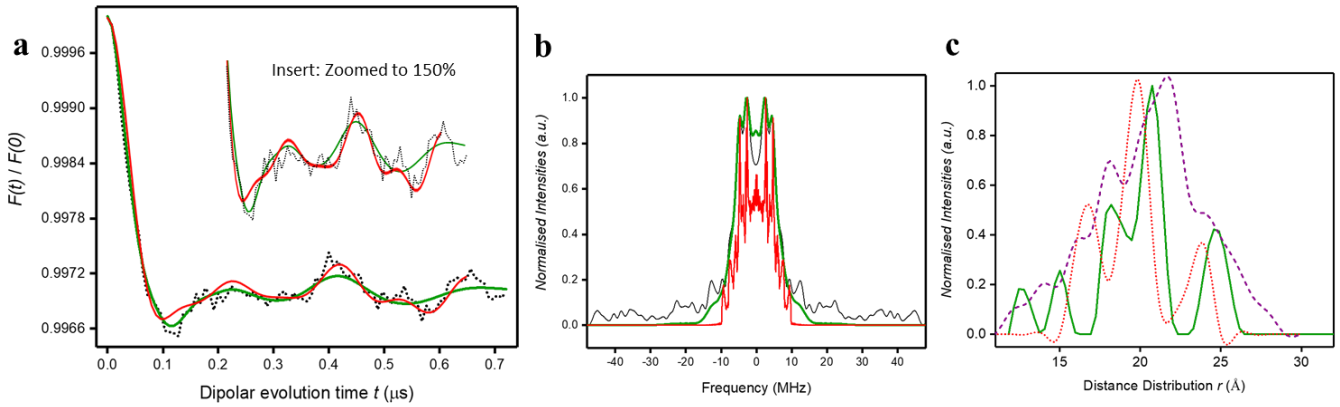

Figure 5. a) Q-Band experimental DEER trace of **4**, after background subtraction, (black crosses, 0.2 mM solution in dry and degassed toluene at 3 K) and fitted data; using DeerAnalysis (solid green line) and using an iterative orientation procedure (solid red line), with vertical enlargement (insert). A four-pulse DEER sequence was used, with the ELDOR pulse at the {Cr_7Ni} maximum (B_0 = 1373 mT) and observation pulse positioned at +100 MHz. Pulse lengths were 20 and 40 ns for π/2 and π, respectively, with τ_1 = 200 ns and τ_2 = 1000 ns. b) Pake pattern from Fourier transformation of dipolar evolution (solid black line); fitted data using DeerAnalysis (solid green line) and the iterative orientation procedure (solid red line). c) Distance distribution using Tikhonov regularizations in DeerAnalysis and corrected *g*-values (solid green line), and from the model from the iterative orientation procedure showing inter-ring metal-metal distances (dashed purple line) and ring centroid-centroid distances (dotted red line).

It is not possible to probe the {Cr_7Ni}…{$CrNi_2$} interactions by DEER due to the very different *g*-values leading to spectra that do not overlap and the limited bandwidth of the resonator used (ca. 200 MHz when over-coupled).

Discussion

The c.w. EPR spectra prove unambiguously that there is no scrambling of metal ions in either the {Cr_7Ni} or {$CrNi_2$} components in **3** or **4**. We only observe the S = ½ ground states of either component which arises from internal antiferromagnetic coupling. Any scrambling of the metal ions would lead to the observation of other spin states. There is no evidence of spin…spin interaction between the {Cr_7Ni} and {$CrNi_2$} components in the c.w. EPR data, hence any interaction must be very weak with respect to the intrinsic linewidths. The c.w. EPR spectra of **3** and **4** are very similar in powder and frozen solution. However, given the lack of resolution of any interaction, this does not prove that the structure is stable in solution (only that the separate components are stable). This evidence comes from the SAXS and AMDS data, and also from DEER measurements that reveal {Cr_7Ni}…{Cr_7Ni} interactions.

The weak coupling regime between {Cr_7Ni} or {$CrNi_2$} is further proven from electron spin relaxation measurements on the separate components.

Electron Spin Relaxation: The T_1 and T_m values for the {Cr_7Ni} components of **3** and **4** (ca. 60-100 μs and 700-800 ns, respectively, at 3 K) are in the range observed for the free ring and in other supramolecular assemblies containing this fragment (Table 2; some caution needs to be taken when comparing data measured at Q- and X-band).[14] Hence, there seems to be relatively little variation in the {Cr_7Ni} relaxation regardless of the complexity of the supramolecular structure (we have measured similar T_m in a complex bearing twelve {Cr_7Ni} rings).[10]

The T_1 and T_m values for the {$CrNi_2$} components of **3** and **4** are ca. 110 - 260 μs and 600 - 700 ns, respectively. Measurements on the isolated {$CrNi_2$} complex [$CrNi_2F(O_2C^tBu)_6(py)_3$] (**5**) under the same conditions give T_1 ca. 800 μs, and T_m ca. 800 ns; we have chosen this complex to give a direct comparison with the pyridyl-terminated {$CrNi_2$} units in **3** and **4**. Hence, in contrast to {Cr_7Ni}, incorporating {$CrNi_2$} into the supramolecular structures **3** and **4** results in a significant decrease in T_1.

In the free complexes, T_1 for {Cr_7Ni} (ca. 100 μs) is significantly shorter than that of {$CrNi_2$} (ca. 800 μs). Both compounds are antiferromagnetically coupled Cr^{III}…Ni^{II} clusters that give rise to S = ½ ground states. {Cr_7Ni} is a much bigger spin system hence has a higher density of spin states, while the exchange coupling within {$CrNi_2$} is weaker[15] leading to lower lying excited states. It would appear that the former is the dominant effect in determining the relative magnitude of T_1 in these two species. The difference between the T_1 times of the two components is much reduced in **3** and **4**. The effect of a fast relaxing spin on a slower relaxing spin depends on the relative magnitude of the coupling and the difference in resonance frequency.[32] Even where the coupling is weak it can enhance the $1/T_1$ relaxation rate of the slow spin. This appears to be the case in **3** and **4**, where T_1 of the {$CrNi_2$} components (110-260 μs) is still longer than that of the {Cr_7Ni} rings (60-100 μs), but reduced from the free {$CrNi_2$}. This is also the reason for the stability of the {Cr_7Ni} T_1 values across a wide range of supramolecular assemblies: in all these systems the rings are the fastest relaxing components.

The T_m values for the slower relaxing {$CrNi_2$} components in both **3** and **4** (600-700 ns) are similar to isolated {$CrNi_2$} (800 ns). This implies that the $1/T_1$ relaxation rate of the faster relaxing {Cr_7Ni} spin (of the order 10^{-1} MHz) is still slow with respect to the interaction frequency.[33] This is consistent with MHz-scale coupling between the components of **3** and **4** (see DEER section).

Note that low-frequency ESEEM effects (< 10 MHz) are observed in the primary echo decay experiments of **3** and **4** when monitoring the {$CrNi_2$} components (20 and 40 ns π/2 and π pulses, respectively), but not on the {Cr_7Ni} components. The fact that they are only observed on the {$CrNi_2$} resonances implies that they are due to the ^{14}N of the {$CrNi_2$}-bound pyridyl groups (Larmor frequency 3.03 MHz at B_0 = 983 mT).

Structures in three phases and at three temperatures

DEER spectroscopy gives us spin…spin distances at 3 K in a dilute frozen solution. Triangular, organic three-spin systems have been studied previously by DEER (with one arm missing in the biradical system), and the effect of three-spin correlations on the distance distribution data examined by comparison to equivalent two-spin molecules, where one arm of the triangle is missing.[31, 34] In **3** and **4**, we have analogues of such systems but based on delocalised multi-centre spin systems. Here we are measuring {Cr_7Ni} ring…ring contacts. From the AMDS calculations we also have a structure in a mobile solution at 300 K (confirmed by the SAXS measurement, Figure 2). From single crystal diffraction we have a structure at 200 K in a crystalline material. It is interesting to compare these three structures of **3** and **4** (Figure 6, Table 3).

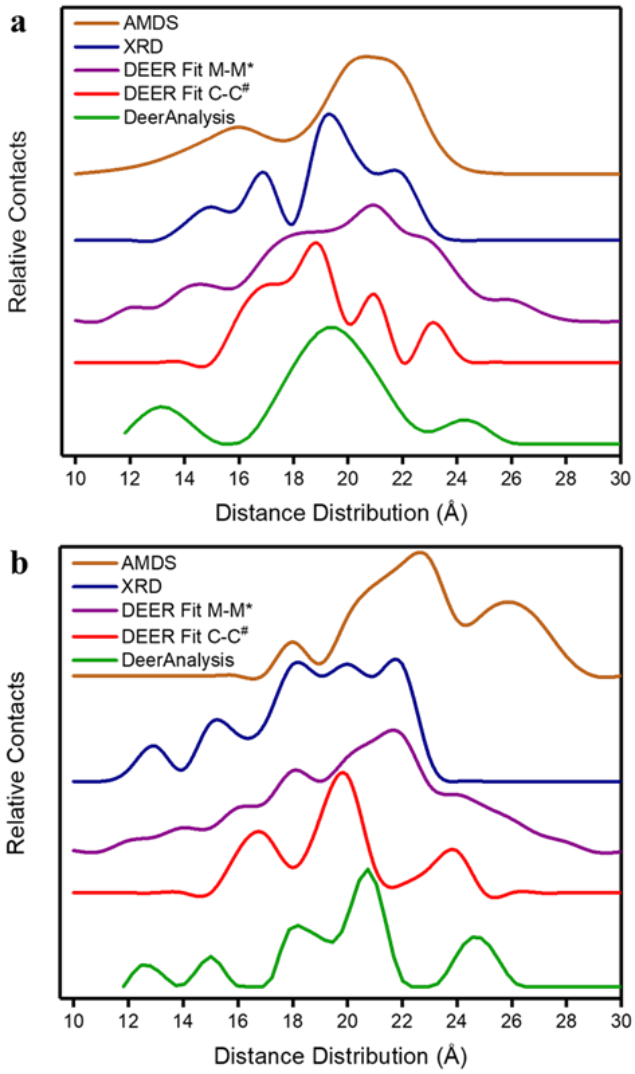

Figure 6. The distribution of inter-{Cr_7Ni} metal...metal contacts by three methods, in (a) **3** and (b) **4**. AMDS calculation (brown); XRD (dark blue); metal-to-metal (purple) and centroid-to-centroid (red) distances found by iterative fit of DEER data; fit from DeerAnalysis (Tikhonov regularizations; green). The AMDS distances were calculated using the centre of mass of the atoms involved and calculated for every timestep over 10 ns; the average was then taken throughout the simulation to determine the distances. The XRD distances between metal ions for each {Cr_7Ni}…{Cr_7Ni} are plotted in 0.5 Å increments using a spline function. The DEER data are taken directly from the distance distributions in Figures 4 and 5.

We make the assumption that the electron spin on the {Cr_7Ni} rings in **3** and **4** sits on the metal sites. The DEER analysis is therefore giving us the distribution of inter-ring M…M distances in frozen solution at 3 K. We are not seeing any

metal…metal contacts involving the central {$CrNi_2$} triangle (see above). We first used DeerAnalysis software[27] using Tikhonov regularisations,[26] to calculate a distance distribution based on dipolar coupling. DeerAnalysis assumes an average nitroxide *g*-value, and a correction factor is required based upon the *g*-values of the experimental pump and observation pulses (1.76 and 1.77, respectively): this results in shifts to slightly shorter distances. The more significant difference here is that the spin on each {Cr_7Ni} ring is distributed across eight sites.[35] Therefore in **3** we have contacts between three sets of eight sites and in **4** we have contacts between two sets of eight sites. Such effects can lead to deviations in distance distributions based on point-dipole models and the cluster centroids, as has been shown with biological FeS clusters.[36]

	Table 3. Maxima (Å) in distribution of intra-ring M…M distances. (a) M…M DEER fit, (b) DeerAnalysis							
3	AMDS	16.0	20.7					
	XRD	15.0	16.9	19.3	21.1			
	DEER[a]	12.1	14.5	17.9	20.9	22.9	26.0	
	DEER[b]	13.1	19.4	24.4				
4	AMDS	18.0	22.7	26.9				
	XRD	12.9	15.2	18.2	20.0	21.8		
	DEER[a]	12.0	13.9	16.0	18.0	21.7	24.2	25.8
	DEER[b]	12.7	15.0	18.1	20.7	24.7		

Hence, we also fit the DEER data with a structural model, allowing for distribution of the spin over the eight sites of the {Cr_7Ni} rings and accounting for orientation selection due to the *g*-anisotropy. In Figures 4(c) and 5(c), we compare the distance distributions extracted from the conformer library, presented both as M…M distances and as ring centroid…centroid distances, with those obtained from model-free DeerAnalysis. It is striking that, for both **3** and **4**, the DEER fit centroid…centroid distribution strongly resembles the DeerAnalysis results in terms of the dominant distances, with the exception that the DeerAnalysis distributions (a) are shifted to longer distances by 1-2 Å, and (b) pick up short distances (< 15 Å) that are not found in the centroid…centroid distribution.

The agreement, despite the neglect of DEER orientation selectivity in {Cr_7Ni} due to *g*-aniostropy,[25] is because the rings are essentially axially symmetric and we are pumping at $g_{x,y}$. In this case we will always detect the perpendicular component of the dipolar coupling pattern, such that a single DEER measurement can yield reasonable distance distributions obtained from Tikhonov regularizations.[28, 37] We have tested and validated this assumption by simulation (see SI).

For both **3** and **4**, the DEER fit M…M distance distributions are broader than either the centroid…centroid or DeerAnalysis results, notably picking up the shorter distances (< 15 Å) and extending to longer distances (> 25 Å). The closer agreement between the DeerAnalysis and DEER fit centroid…centroid distributions is likely a result of the fact that DeerAnalysis uses the point dipole approach, and given that the spin is evenly distributed around the {Cr_7Ni} ring (once positional disorder of the Ni(II) ion is considered) this seems to average out to give distances similar to a spin localised at the centre of the ring.

For **3** the distance distribution from DeerAnalysis has three maxima (Figure 6a), at 13.1 Å (towards the lower end of distances that can be measured by DEER),[38, 39] a dominant peak at 19.4 Å, and a smaller peak at around 24.4 Å. The DEER fit M…M distribution gives peaks between 12 and 26 Å, with the bulk of contacts between 18-24 Å (Figure 6a).

To compare this with the inter-ring M…M distances in **3** as observed by single crystal X-ray diffraction we have arranged the M…M distances from diffraction in distributions of 0.5 Å and then broadened the distribution (dark blue line in Figure 6a). There are two maxima at 15.0 and 16.9 Å, reflecting the rings being arranged in an isosceles triangle in the crystal. There is then a gap in the distribution before we reach a maximum at 19.3 Å, consistent with the broad maximum in the DEER fit M…M data and the maximum in the DeerAnalysis distribution. There is then a small fall before a peak at 21.1 Å.

If we then compare with the AMDS structure (brown line in Figure 6a) we see a very similar shape to the DeerAnalysis distribution, but shifted to longer distances with two maxima at 16.0 and 20.7 Å. The simpler distribution from AMDS *cf*. XRD suggests that the structure in fluid solution is relaxing to an equilateral triangle of rings compared to the crystal structure. The DEER fit M…M distribution is more complex, with shorter and longer distances, reflecting the fact that a number of conformations are trapped on freezing the solution, and there are also possible differences in librational effects due to the extreme difference in temperatures of measurement (3 and 300 K). Some of this detail is lost in the simpler DeerAnalysis treatment. However, the dominant DEER fit M…M distances around 21 Å agree with that from AMDS.

The conclusion is that in fluid solution at room temperature **3** has a structure where the rings in the three [2]rotaxanes form an equilateral triangle. Additional structure is seen in the XRD as packing leads to a change in the overall structure towards an isosceles triangle, but with similar size. While a range of conformations are found in the frozen solution at 3 K, the dominant distances are similar to the fluid solution.

For compound **4** the result is very different (Figure 6b). The XRD distance distribution has a similar longest distance at 22 Å, *cf*. 21 Å for **3**. However, there are significantly shorter contacts at 13 Å, *cf*. 15 Å in **3**. In **4** the AMDS and XRD structures are radically different from one another. In AMDS the shortest contact has a maximum at 18.0 Å, with the shortest contacts found in XRD and DEER (see below) entirely missing. The majority of M…M contacts by AMDS are around 22.7 Å, around the longest contact from XRD and the dominant contact by DEER fit. Finally, the AMDS has a much longer and significant contact at above 26 Å which is absent in the XRD. Hence, the AMDS structure is much more extended than the structure as observed by crystallography.

The DeerAnalysis distance distribution for **4** gives short distances at 12.7 and 15.0 Å, the majority of contacts from 17.5-21.9 Å, and a long-distance peak at 24.7 Å. The DEER fit M…M distribution gives peaks between shortest and longest distances of 12 and 28 Å, with the dominant peak at around 22 Å. Comparing these to equivalent data for **3**, both analyses show that in **4** there is a broader distance distribution, extending to longer distances, in the frozen solution. The DEER fit M…M distribution for **4** appears to combine features of those from the XRD and AMDS, with the short distances from the former and the long distances from the latter. However, although the M…M DEER fit result contains distances that extend beyond those found in the AMDS distributions, the dominant distance is significantly shorter.

All these results say that the [3]-rotaxane (**4**) relaxes much more in solution than the [4]-rotaxane (**3**). The presence of only

two large [2]rotaxanes attached to the central triangle in **4** leads to steric repulsion between these groups. The result is a bigger structure in mobile solution (also shown by the radius of gyration data, see SI) and also a broader range of conformations on freezing the solutions as shown by DEER. Hence, the fluid and frozen solution structures differ more significantly from each other for **4** than for **3**.

Conclusion

We have prepared two large supramolecular assemblies **3** and **4**, containing twenty-seven and twenty-one paramagnetic centres respectively. Single crystal diffraction studies allow us to show these are [4]- and [3]rotaxanes with three or two {Cr_7Ni} rings attached to a central {$CrNi_2$} triangle.

Such huge molecules have many degrees of freedom and by analysing AMDS structures calculated in solution, confirmed by SAXS data, we can see that the symmetric [4]rotaxane behaves very differently from the asymmetric [3]rotaxane. The packing of the [4]rotaxane in the crystal leads to an isosceles triangle of {Cr_7Ni} rings that is not seen in solution by SAXS/AMDS. Here the crystallography establishes connectivity but not the conformation in solution, while DEER shows a relatively narrow range of conformations in the frozen solution. For the asymmetric [3]rotaxane we find that the structural differences in solution, fluid and frozen, are much greater in terms of both the extension of the molecule and the range of conformations observed.

Determining such details of the structure of very large paramagnetic assemblies is very difficult as the line broadening due to paramagnetism vitiates the use of NMR spectroscopy. Here the combination of AMDS and DEER allows us to characterise the materials and their conformers from 3 to 300 K.

ASSOCIATED CONTENT

Supporting Information. Experimental section; crystallography; c.w. EPR data; EDFS data: relaxation data; M…M distance distribution from XRD; SAXS data; DEER modelling including orientation selection effects and structural model fitting; multi-spin analysis. This material is available free of charge via the Internet at http://pubs.acs.org.

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The manuscript was written through contributions of all authors. All authors have given approval to the final version of the manuscript.

Funding Sources

This work was supported by the EPSRC through the award of a doctoral training grant to SJL and funding of the EPSRC National EPR Facility at Manchester (NS/A000055/1). This work was supported by the EPSRC(UK) (grant number EP/L018470/1) and a Established Career Fellowship (EP/R011079/1) to REPW, We also thank EPSRC (UK) for funding an X-ray diffractometer (EP/K039547/1). We also thank the European Research Council for an Advanced Grant (ERC-2017-ADG-786734). We thank Diamond Light Source for access to synchrotron X-ray facilities. AMB thanks the Royal Society and EPSRC for a Dorothy Hodgkin Fellowship (DH160004). We dedicate this paper to Professor Alan J. Welch on the occasion of his retirement.

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